

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number:

10/596,024

Source:

IFW

Date Processed by STIC:

3/20/07

# ***ENTERED***



IFWO

## RAW SEQUENCE LISTING

DATE: 03/20/2007

PATENT APPLICATION: US/10/596,024

TIME: 15:02:12

Input Set : N:\efs\03\_20\_07\10596024\_efs\PAT\_989W\_2\_SEQUENCE\_LISTING.txt

Output Set: N:\CRF4\03202007\J596024.raw

3 <110> APPLICANT: MIETKIEWSKA, Elzbieta et al.

5 <120> TITLE OF INVENTION: FATTY ACID ELONGASE (FAE) GENES AND THEIR UTILITY IN INCREASING

6 ERUCIC ACID AND OTHER VERY LONG-CHAIN FATTY ACID PROPORTIONS IN

7 SEED OIL

9 <130> FILE REFERENCE: PAT 989W-2

11 <140> CURRENT APPLICATION NUMBER: US 10/596,024

C--> 12 <141> **CURRENT FILING DATE: 2006-05-25**

14 <150> PRIOR APPLICATION NUMBER: US 60/524;645

15 <151> PRIOR FILING DATE: 2003-11-25

17 <160> NUMBER OF SEQ ID NOS: 27

19 <170> SOFTWARE: PatentIn version 3.2

21 <210> SEQ ID NO: 1

22 <211> LENGTH: 18

23 <212> TYPE: DNA

24 <213> ORGANISM: Artificial

26 <220> FEATURE:

27 <223> OTHER INFORMATION: F1 Forward Primer

29 <400> SEQUENCE: 1

31 tctwggwggm atgggttg 18

34 <210> SEQ ID NO: 2

35 <211> LENGTH: 6

36 <212> TYPE: PRT

37 <213> ORGANISM: Artificial

39 <220> FEATURE:

40 <223> OTHER INFORMATION: Coded by F1 Forward Primer

42 <400> SEQUENCE: 2

44 Leu Gly Gly Met Gly Cys

45 1 5

48 <210> SEQ ID NO: 3

49 <211> LENGTH: 18

50 <212> TYPE: DNA

51 <213> ORGANISM: Artificial

53 <220> FEATURE:

54 <223> OTHER INFORMATION: R1 Reverse Primer

56 <400> SEQUENCE: 3

58 trtaygcyar ctctacc 18

61 <210> SEQ ID NO: 4

62 <211> LENGTH: 6

63 <212> TYPE: PRT

64 <213> ORGANISM: Artificial

66 <220> FEATURE:

67 <223> OTHER INFORMATION: Coded by R1 Reverse Primer

69 <400> SEQUENCE: 4

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71 Trp Tyr Glu Leu Ala Tyr
72 1          5
75 <210> SEQ ID NO: 5
76 <211> LENGTH: 20
77 <212> TYPE: DNA
78 <213> ORGANISM: Artificial
80 <220> FEATURE:
81 <223> OTHER INFORMATION: P Forward Primer
83 <400> SEQUENCE: 5
85 accatgtcag gaacaaaagc
88 <210> SEQ ID NO: 6
89 <211> LENGTH: 23
90 <212> TYPE: DNA
91 <213> ORGANISM: Artificial
93 <220> FEATURE:
94 <223> OTHER INFORMATION: PR Reverse Primer
96 <400> SEQUENCE: 6
98 ttaatttaat ggaacctcaa ccg
101 <210> SEQ ID NO: 7
102 <211> LENGTH: 32
103 <212> TYPE: DNA
104 <213> ORGANISM: Artificial
106 <220> FEATURE:
107 <223> OTHER INFORMATION: F2 Forward Primer
109 <400> SEQUENCE: 7
111 tcgaggatgt cgcttcaccg atttggaac ac
114 <210> SEQ ID NO: 8
115 <211> LENGTH: 33
116 <212> TYPE: DNA
117 <213> ORGANISM: Artificial
119 <220> FEATURE:
120 <223> OTHER INFORMATION: R2 Reverse Primer
122 <400> SEQUENCE: 8
124 gtttccaaat cggtgaagcg acatcctcga tgg
127 <210> SEQ ID NO: 9
128 <211> LENGTH: 25
129 <212> TYPE: DNA
130 <213> ORGANISM: Artificial
132 <220> FEATURE:
133 <223> OTHER INFORMATION: F3 Forward Primer
135 <400> SEQUENCE: 9
137 taggatccat gtcaggaaca aaagc
140 <210> SEQ ID NO: 10
141 <211> LENGTH: 30
142 <212> TYPE: DNA
143 <213> ORGANISM: Artificial
145 <220> FEATURE:
146 <223> OTHER INFORMATION: R3 Reverse Primer
148 <400> SEQUENCE: 10

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150 tagagctctt aatttaatgg aacctcaacc 30
153 <210> SEQ ID NO: 11
154 <211> LENGTH: 30
155 <212> TYPE: DNA
156 <213> ORGANISM: Artificial
158 <220> FEATURE:
159 <223> OTHER INFORMATION: R4 Reverse Primer
161 <400> SEQUENCE: 11
163 taggatacctt aatttaatgg aacctcaacc 30
166 <210> SEQ ID NO: 12
167 <211> LENGTH: 17
168 <212> TYPE: DNA
169 <213> ORGANISM: Artificial
171 <220> FEATURE:
172 <223> OTHER INFORMATION: F4 Forward Primer
174 <400> SEQUENCE: 12
176 atgtcaggaa caaaagc 17
179 <210> SEQ ID NO: 13
180 <211> LENGTH: 22
181 <212> TYPE: DNA
182 <213> ORGANISM: Artificial
184 <220> FEATURE:
185 <223> OTHER INFORMATION: R5 Reverse Primer
187 <400> SEQUENCE: 13
189 taatttaatg gaacctcaac cg 22
192 <210> SEQ ID NO: 14
193 <211> LENGTH: 24
194 <212> TYPE: DNA
195 <213> ORGANISM: Artificial
197 <220> FEATURE:
198 <223> OTHER INFORMATION: F5 Forward Primer
200 <400> SEQUENCE: 14
202 gcaatgacgt ccattaacgt aaag 24
205 <210> SEQ ID NO: 15
206 <211> LENGTH: 21
207 <212> TYPE: DNA
208 <213> ORGANISM: Artificial
210 <220> FEATURE:
211 <223> OTHER INFORMATION: R6 Reverse Primer
213 <400> SEQUENCE: 15
215 ttaggaccga ccgttttggg c 21
218 <210> SEQ ID NO: 16
219 <211> LENGTH: 29
220 <212> TYPE: DNA
221 <213> ORGANISM: Artificial
223 <220> FEATURE:
224 <223> OTHER INFORMATION: F6 Forward Primer
226 <400> SEQUENCE: 16
228 tatctagaat gacgtccatt aacgtaaag 29

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231 <210> SEQ ID NO: 17
232 <211> LENGTH: 27
233 <212> TYPE: DNA
234 <213> ORGANISM: Artificial
236 <220> FEATURE:
237 <223> OTHER INFORMATION: R7 Reverse Primer
239 <400> SEQUENCE: 17
241 atggtacctt aggaccgacc gttttgg                27
244 <210> SEQ ID NO: 18
245 <211> LENGTH: 22
246 <212> TYPE: DNA
247 <213> ORGANISM: Artificial
249 <220> FEATURE:
250 <223> OTHER INFORMATION: NN-3 Primer
252 <400> SEQUENCE: 18
254 tttcttcgcc acttgtcact cc                22
257 <210> SEQ ID NO: 19
258 <211> LENGTH: 21
259 <212> TYPE: DNA
260 <213> ORGANISM: Artificial
262 <220> FEATURE:
263 <223> OTHER INFORMATION: NN-4 Primer
265 <400> SEQUENCE: 19
267 cgcgctatat tttgttttct a                21
270 <210> SEQ ID NO: 20
271 <211> LENGTH: 32
272 <212> TYPE: DNA
273 <213> ORGANISM: Artificial
275 <220> FEATURE:
276 <223> OTHER INFORMATION: OM087 Primer
278 <400> SEQUENCE: 20
280 agagagaggg atccatgagt gtgataggta gg                32
283 <210> SEQ ID NO: 21
284 <211> LENGTH: 33
285 <212> TYPE: DNA
286 <213> ORGANISM: Artificial
288 <220> FEATURE:
289 <223> OTHER INFORMATION: OM088 Primer
291 <400> SEQUENCE: 21
293 gaggaagaag gatccgggtc tatatactac tct                33
296 <210> SEQ ID NO: 22
297 <211> LENGTH: 503
298 <212> TYPE: PRT
299 <213> ORGANISM: Tropaeolum majus
301 <400> SEQUENCE: 22
303 Met Ser Gly Thr Lys Ala Thr Ser Val Ser Val Pro Leu Pro Asp Phe
304 1                    5                    10                    15
306 Lys Gln Ser Val Asn Leu Lys Tyr Val Lys Leu Gly Tyr His Tyr Ser
307                20                    25                    30

```

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309 Ile Thr His Ala Met Tyr Leu Phe Leu Thr Pro Leu Leu Leu Ile Met
310      35      40      45
312 Ser Ala Gln Ile Ser Thr Phe Ser Ile Gln Asp Phe His His Leu Tyr
313      50      55      60
315 Asn His Leu Ile Leu His Asn Leu Ser Ser Leu Ile Leu Cys Ile Ala
316 65      70      75      80
318 Leu Leu Leu Phe Val Leu Thr Leu Tyr Phe Leu Thr Arg Pro Thr Pro
319      85      90      95
321 Val Tyr Leu Leu Asn Phe Ser Cys Tyr Lys Pro Asp Ala Ile His Lys
322      100     105     110
324 Cys Asp Arg Arg Arg Phe Met Asp Thr Ile Arg Gly Met Gly Thr Tyr
325      115     120     125
327 Thr Glu Glu Asn Ile Glu Phe Gln Arg Lys Val Leu Glu Arg Ser Gly
328      130     135     140
330 Ile Gly Glu Ser Ser Tyr Leu Pro Pro Thr Val Phe Lys Ile Pro Pro
331 145      150     155     160
333 Arg Val Tyr Asp Ala Glu Glu Arg Ala Glu Ala Glu Met Leu Met Phe
334      165     170     175
336 Gly Ala Val Asp Gly Leu Phe Glu Lys Ile Ser Val Lys Pro Asn Gln
337      180     185     190
339 Ile Gly Val Leu Val Val Asn Cys Gly Leu Phe Asn Pro Ile Pro Ser
340      195     200     205
342 Leu Ser Ser Met Ile Val Asn Arg Tyr Lys Met Arg Gly Asn Val Phe
343      210     215     220
345 Ser Tyr Asn Leu Gly Gly Met Gly Cys Ser Ala Gly Val Ile Ser Ile
346 225     230     235     240
348 Asp Leu Ala Lys Asp Leu Leu Gln Val Arg Pro Asn Ser Tyr Ala Leu
349      245     250     255
351 Val Val Ser Leu Glu Cys Ile Ser Lys Asn Leu Tyr Leu Gly Glu Gln
352      260     265     270
354 Arg Ser Met Leu Val Ser Asn Cys Leu Phe Arg Met Gly Gly Ala Ala
355      275     280     285
357 Ile Leu Leu Ser Asn Lys Met Ser Asp Arg Trp Arg Ser Lys Tyr Arg
358      290     295     300
361 Leu Val His Thr Val Arg Thr His Lys Gly Thr Glu Asp Asn Cys Phe
362 305      310     315     320
364 Ser Cys Val Thr Arg Lys Glu Asp Ser Asp Gly Lys Ile Gly Ile Ser
365      325     330     335
367 Leu Ser Lys Asn Leu Met Ala Val Ala Gly Asp Ala Leu Lys Thr Asn
368      340     345     350
370 Ile Thr Thr Leu Gly Pro Leu Val Leu Pro Met Ser Glu Gln Leu Leu
371      355     360     365
373 Phe Phe Ala Thr Leu Val Gly Lys Lys Val Phe Lys Met Lys Leu Gln
374      370     375     380
376 Pro Tyr Ile Pro Asp Phe Lys Leu Ala Phe Glu His Phe Cys Ile His
377 385      390     395     400
379 Ala Gly Gly Arg Ala Val Leu Asp Glu Leu Glu Lys Asn Leu Lys Leu
380      405     410     415
382 Ser Ser Trp His Met Glu Pro Ser Arg Met Ser Leu Tyr Arg Phe Gly

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## RAW SEQUENCE LISTING ERROR SUMMARY

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21

**VERIFICATION SUMMARY**

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date